

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/540,516
Source: IFWP
Date Processed by STIC: 2/22/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/540,516

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 02/22/2007

PATENT APPLICATION: US/10/540,516

TIME: 12:21:16

Input Set : A:\Q88805.ST25.txt

Output Set: N:\CRF4\02222007\J540516.raw

3 <110> APPLICANT: Imstar Image et Modelisation: Strategie, Analyse et
 4 Realisation
 5 Soussaline, Francoise
 6 Khomyakova, Elena
 8 <120> TITLE OF INVENTION: Chip Reader For Biochips and Associated Methods
 10 <130> FILE REFERENCE: Q88805
 12 <140> CURRENT APPLICATION NUMBER: 10/540,516
 13 <141> CURRENT FILING DATE: 2005-06-23
 15 <150> PRIOR APPLICATION NUMBER: PCT/FR2003/003886
 16 <151> PRIOR FILING DATE: 2003-12-23
 18 <150> PRIOR APPLICATION NUMBER: WO 2004/059302 A1
 19 <151> PRIOR FILING DATE: 2004-07-15
 21 <160> NUMBER OF SEQ ID NOS: 33
 23 <170> SOFTWARE: PatentIn version 3.3
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 24
 27 <212> TYPE: DNA
 28 <213> ORGANISM: probe *invalid response - see item 10*
 30 <400> SEQUENCE: 1 *on Ena summary sheet*
 31 taggaaacac caaagatgat attt 24
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 24
 36 <212> TYPE: DNA
 37 <213> ORGANISM: probe
 39 <400> SEQUENCE: 2
 40 cataggaaac accaatgata tttt 24
 43 <210> SEQ ID NO: 3
 44 <211> LENGTH: 21
 45 <212> TYPE: DNA
 46 <213> ORGANISM: probe
 48 <400> SEQUENCE: 3
 49 aggaaaactg agaacagaat g 21
 52 <210> SEQ ID NO: 4
 53 <211> LENGTH: 21
 54 <212> TYPE: DNA
 55 <213> ORGANISM: probe
 57 <400> SEQUENCE: 4
 58 aggaaaacta agaacagaat g 21
 61 <210> SEQ ID NO: 5
 62 <211> LENGTH: 21
 63 <212> TYPE: DNA
 64 <213> ORGANISM: probe
 66 <400> SEQUENCE: 5

see pp 1-5
 Does Not Comply
 Corrected Diskette Needed

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Input Set : A:\Q88805.ST25.txt

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79	<210> SEQ ID NO: 7	
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81	<212> TYPE: DNA	
82	<213> ORGANISM: probe	
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85	accttctcaa agaactatat tg	22
88	<210> SEQ ID NO: 8	
89	<211> LENGTH: 22	
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91	<213> ORGANISM: probe	
93	<400> SEQUENCE: 8	
94	accttctcta agaactatat tg	22
97	<210> SEQ ID NO: 9	
98	<211> LENGTH: 17	
99	<212> TYPE: DNA	
100	<213> ORGANISM: probe	
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107	<211> LENGTH: 17	
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138	<400> SEQUENCE: 13	
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Input Set : A:\Q88805.ST25.txt

Output Set: N:\CRF4\02222007\J540516.raw

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154 <213> ORGANISM: probe
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157 accttctcca agaac 15
160 <210> SEQ ID NO: 16
161 <211> LENGTH: 15
162 <212> TYPE: DNA
163 <213> ORGANISM: probe
165 <400> SEQUENCE: 16
166 accttctcaa agaac 15
169 <210> SEQ ID NO: 17
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172 <213> ORGANISM: probe
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180 <212> TYPE: DNA
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184 cttgctcggt gacct 15
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188 <211> LENGTH: 15
189 <212> TYPE: DNA
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196 <210> SEQ ID NO: 20
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198 <212> TYPE: DNA
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214 <210> SEQ ID NO: 22

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RAW SEQUENCE LISTING

DATE: 02/22/2007

PATENT APPLICATION: US/10/540,516

TIME: 12:21:17

Input Set : A:\Q88805.ST25.txt

Output Set: N:\CRF4\02222007\J540516.raw

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232 <210> SEQ ID NO: 24	
233 <211> LENGTH: 24	
234 <212> TYPE: DNA	
235 <213> ORGANISM: probe	
237 <400> SEQUENCE: 24	
238 aaatatcatc ttggtgttt ccta	24
241 <210> SEQ ID NO: 25	
242 <211> LENGTH: 24	
243 <212> TYPE: DNA	
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255 <400> SEQUENCE: 26	
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259 <210> SEQ ID NO: 27	
260 <211> LENGTH: 21	
261 <212> TYPE: DNA	
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268 <210> SEQ ID NO: 28	
269 <211> LENGTH: 18	
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273 <400> SEQUENCE: 28	
274 aatatacttg gagaaggt	18
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280 <213> ORGANISM: probe	
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286 <210> SEQ ID NO: 30	
287 <211> LENGTH: 17	

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DATE: 02/22/2007

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TIME: 12:21:17

Input Set : A:\Q88805.ST25.txt

Output Set: N:\CRF4\02222007\J540516.raw

288 <212> TYPE: DNA
289 <213> ORGANISM: probe
291 <400> SEQUENCE: 30
292 aggtcaacga gcaagaa 17
295 <210> SEQ ID NO: 31
296 <211> LENGTH: 17
297 <212> TYPE: DNA
298 <213> ORGANISM: probe
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304 <210> SEQ ID NO: 32
305 <211> LENGTH: 17
306 <212> TYPE: DNA
307 <213> ORGANISM: probe
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310 tgagtggagg tcaacga 17
313 <210> SEQ ID NO: 33
314 <211> LENGTH: 17
315 <212> TYPE: DNA
316 <213> ORGANISM: probe
318 <400> SEQUENCE: 33
319 tgagtggaga tcaacga 17

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/540,516

DATE: 02/22/2007

TIME: 12:21:18

Input Set : A:\Q88805.ST25.txt

Output Set: N:\CRF4\02222007\J540516.raw